Amendments to the Claims:

This listing of claims replaces and supercedes all prior versions, and listings, of claims in the application:

Listing of the Claims:

1. (Currently Amended) Method to distinguish, whether an event sequence on a molecular level is a memory driven event sequence or is not a memory driven event sequence on a time scale T_1 to T_2, where $T_1 < T_2$ are arbitrary times, characterized in that

a) the first order autocorrelation function $G(\tau)$ of the event sequence is calculated,

b) the second order autocorrelation function $G(\tau_1, \tau_2)$ of the event sequence is calculated,

c) it is decided that the event sequence is a memory driven event sequence on the time scale T_1 to T_2,

if the second order autocorrelation function of the event sequence can be expressed within approximately five percent ~~experimental error~~ as the product of first order autocorrelation functions, i.e. $G(\tau_1, \tau_2) = G(\tau_1) * G(\tau_2)$ for $T_1 < \tau_1, \tau_2 < T_2$, and

d) it is decided that the event sequence is not a memory driven event sequence on the time scale T_1 to T_2,

if the second order autocorrelation function of the event sequence cannot be expressed within approximately 5% ~~experimental error~~ as the product of first order autocorrelation functions, i.e., $G(\tau_1, \tau_2) \neq G(\tau_1)*G(\tau_2)$ for $T_1 < \tau_1$, $T_2 < T_2$.

2. (Original) Method according to claim 1,
characterized in that

a. the first order autocorrelation function $G(\tau)$ of the event sequence is calculated as:

$$G(\tau) \equiv \frac{E(X_0 X_\tau)}{E(X_0)E(X_\tau)}$$

where X is the random variable that describes the event and E(.) denotes the expectation value,

b) the second order autocorrelation function $G(\tau_1,\tau_2)$ of the event sequence is calculated as:

$$G(\tau_1, \tau_2) \equiv \frac{E(X_0 X_{\tau_1} X_{\tau_1+\tau_2})}{E(X_0)E(X_{\tau_1})E(X_{\tau_1+\tau_2})}$$

where X is the random variable that describes the event and E(.) denotes

the expectation value,

3. (Original) Method according to claim 1, characterized in that the degree of memory of the system is quantified by the non-Markovian function NMF calculated according to:

$$NMF(\tau_1,\tau_2) = P_f(\frac{G(\tau_1,\tau_2)}{G(\tau_2)} - G(\tau_1))$$

where p_f is the probability of the event X at a particular time.

4. (Original) Method according to claim 1,
characterized in that
the event sequence is a sequence of fluorescence events observed in a confocal microscope.

5. (Original) Method according to claim 4 to discriminate an event sequence from a single molecule against an event sequence from background processes or noise, characterized in that

a) it is decided that the event sequence is due to a single molecule, if it is a memory driven event sequence,

b) it is decided that the event sequence is due to background processes or

noise, if it is a non-memory driven event sequence.

6. (Withdrawn) Method according to claim 5 for single molecule sequencing, **characterized in that**

a) it is decided that the fluorescence events observed are due to nuclease-liberated nucleotides if the sequence of fluorescence events is a memory driven sequence of events and

b) it is decided that the fluorescence events observed are due to contaminating nucleotides or other backgorund signals, if the sequence of fluorescence events is not a memory driven sequence of events.

7. (Withdrawn) Method according to claim 6, characterized in that the fluorescence events are observed in a confocal microscope.

8. (Withdrawn) Method according to claim 6 for analyzing of catalytic complexes, characterized in that

a) it is decided that the fluorescence events observed are due to characteristics of the catalytic complex if the sequence of fluorescence events is a memory driven sequence of events and

b) it is decided that the fluorescence events observed are due to contaminating nucleotides or other background signals, if the sequence of fluorescence events is not a memory driven sequence of events.

9. (Withdrawn) Method according to claim 8, characterized in that the catalytic complex comprises a catalyst, a substrate being converted to a product and optionally a cosubstrate.

10. (Withdrawn) Method according to claim 8, characterized in that the catalyst is selected from biomolecules, e.g. enzymes, inorganic molecules and organic molecules.

11. (Previously Presented) Method according to claim 5 wherein an oscillating process is analyzed.